

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 10 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 15 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1275
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48
 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 1 5 10 15
 25 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC 96
 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30
 30 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG 144
 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45
 35 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA 192
 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 50 55 60
 40 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC 240
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65 70 75 80
 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA 288
 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 85 90 95
 45 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG 336
 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 100 105 110
 50 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC 384
 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125
 55 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC 432
 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 130 135 140
 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG 480
 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
 145 150 155 160

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	TAC	GGA	ATG	CTG	GCC	CGC	CTC	GCC	GTC	GAG	GCC	GGC	TTC	GAC	TGG	GTC	528
	Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
					165					170					175		
5	TAC	TAC	GAG	TCC	AAG	GCG	CAC	ATC	CAC	TGC	TCC	GTC	AAA	GCA	GAA	AAC	576
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	
				180					185					190			
10	TCA	GTG	GCA	GCG	AAA	TCA	GGA	GGC	TGC	TTC	CCT	GGC	TCA	GCC	ACA	GTG	624
	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	
			195					200					205				
15	CAC	CTG	GAG	CAT	GGA	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCT	GGG	672
	His	Leu	Glu	His	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	
			210				215					220					
20	GAC	CGC	GTG	CTG	GCT	GCT	GAC	GCG	GAC	GGC	CGG	CTG	CTC	TAC	AGT	GAC	720
	Asp	Arg	Val	Leu	Ala	Ala	Asp	Ala	Asp	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	
						230					235					240	
25	TTC	CTC	ACC	TTC	CTC	GAC	CGG	ATG	GAC	AGC	TCC	CGA	AAG	CTC	TTC	TAC	768
	Phe	Leu	Thr	Phe	Leu	Asp	Arg	Met	Asp	Ser	Ser	Arg	Lys	Leu	Phe	Tyr	
					245					250					255		
30	GTC	ATC	GAG	ACG	CGG	CAG	CCC	CGG	GCC	CGG	CTG	CTA	CTG	ACG	GCG	GCC	816
	Val	Ile	Glu	Thr	Arg	Gln	Pro	Arg	Ala	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
				260					265					270			
35	CAC	CTG	CTC	TTT	GTG	GCC	CCC	CAG	CAC	AAC	CAG	TCG	GAG	GCC	ACA	GGG	864
	His	Leu	Leu	Phe	Val	Ala	Pro	Gln	His	Asn	Gln	Ser	Glu	Ala	Thr	Gly	
				275				280					285				
40	TCC	ACC	AGT	GGC	CAG	GCG	CTC	TTC	GCC	AGC	AAC	GTG	AAG	CCT	GGC	CAA	912
	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln	
				290			295					300					
45	CGT	GTC	TAT	GTG	CTG	GGC	GAG	GGC	GGG	CAG	CAG	CTG	CTG	CCG	GCG	TCT	960
	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser	
					310					315						320	
50	GTC	CAC	AGC	GTC	TCA	TTG	CGG	GAG	GAG	GCG	TCC	GGA	GCC	TAC	GCC	CCA	1008
	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro	
					325					330					335		
55	CTC	ACC	GCC	CAG	GGC	ACC	ATC	CTC	ATC	AAC	CGG	GTG	TTG	GCC	TCC	TGC	1056
	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	
				340				345						350			
60	TAC	GCC	GTC	ATC	GAG	GAG	CAC	AGT	TGG	GCC	CAT	TGG	GCC	TTC	GCA	CCA	1104
	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro	
				355				360					365				
65	TTC	CGC	TTG	GCT	CAG	GGG	CTG	CTG	GCC	GCC	CTC	TGC	CCA	GAT	GGG	GCC	1152
	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala	
				370			375					380					
70	ATC	CCT	ACT	GCC	GCC	ACC	ACC	ACC	ACT	GGC	ATC	CAT	TGG	TAC	TCA	CGG	1200
	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg	
						390				395					400		
75	CTC	CTC	TAC	CGC	ATC	GGC	AGC	TGG	GTG	CTG	GAT	GGT	GAC	GCG	CTG	CAT	1248
	Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His	

	405	410	415	
	CCG CTG GGC ATG GTG GCA CCG GCC AGC TG			1277
5	Pro Leu Gly Met Val Ala Pro Ala Ser			
	420	425		

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1191

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG	48
	Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
30	GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG	96
	Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
	20 25 30	
35	CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT	144
	Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
	35 40 45	
40	GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG	192
	Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
	50 55 60	
45	GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC	240
	Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
	65 70 75 80	
	TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC	288
	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
	85 90 95	
50	CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC	336
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
	100 105 110	
55	GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC	384
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
60	TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC	432
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
	130 135 140	

5	CGT Arg 145	GCC Ala	TTG Leu	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCT Ser	GAC Asp	CGT Arg	GAC Asp 155	CGT Arg	AAT Asn	AAG Lys	TAT Tyr	GGT Gly 160	480
	TTG Leu	TTG Leu	GCG Ala	CGC Arg	CTA Leu 165	GCT Ala	GTG Val	GAA Glu	GCC Ala	GGA Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAC Tyr	528
10	GAG Glu	TCC Ser	CGC Arg	AAC Asn 180	CAC His	ATC Ile	CAC His	GTA Val	TCG Ser 185	GTC Val	AAA Lys	GCT Ala	GAT Asp	AAC Asn 190	TCA Ser	CTG Leu	576
15	GCG Ala	GTC Val	CGA Arg 195	GCC Ala	GGA Gly	GGC Gly	TGC Cys	TTT Phe 200	CCG Pro	GGA Gly	AAT Asn	GCC Ala	ACG Thr 205	GTG Val	CGC Arg	TTG Leu	624
20	CGG Arg 210	AGC Ser	GGC Gly	GAA Glu	CGG Arg	AAG Lys	GGG Gly 215	CTG Leu	AGG Arg	GAA Glu	CTA Leu	CAT His 220	CGT Arg	GGT Gly	GAC Asp	TGG Trp	672
25	GTA Val 225	CTG Leu	GCC Ala	GCT Ala	GAT Asp	GCA Ala 230	GCG Ala	GGC Gly	CGA Arg	GTG Val	GTA Val 235	CCC Pro	ACG Thr	CCA Pro	GTG Val	CTG Leu 240	720
	CTC Leu	TTC Phe	CTG Leu	GAC Asp	CGG Arg 245	GAT Asp	CTG Leu	CAG Gln	CGC Arg	CGC Arg 250	GCC Ala	TCG Ser	TTC Phe	GTG Val	GCT Ala 255	GTG Val	768
30	GAG Glu	ACC Thr	GAG Glu	CGG Arg 260	CCT Pro	CCG Pro	CGC Arg	AAA Lys	CTG Leu 265	TTG Leu	CTC Leu	ACA Thr	CCC Pro	TGG Trp 270	CAT His	CTG Leu	816
35	GTG Val	TTC Phe	GCT Ala 275	GCT Ala	CGC Arg	GGG Gly	CCA Pro	GCG Ala 280	CCT Pro	GCT Ala	CCA Pro	GGT Gly	GAC Asp 285	TTT Phe	GCA Ala	CCG Pro	864
40	GTG Val 290	TTC Phe	GCG Ala	CGC Arg	CGC Arg	TTA Leu	CGT Arg 295	GCT Ala	GGC Gly	GAC Asp	TCG Ser 300	GTG Val	CTG Leu	GCT Ala	CCC Pro	GGC Gly	912
45	GGG Gly 305	GAC Asp	GCG Ala	CTC Leu	CAG Gln	CCG Pro 310	GCG Ala	CGC Arg	GTA Val	GCC Ala	CGC Arg 315	GTG Val	GCG Ala	CGC Arg	GAG Glu 320	GAA Glu	960
	GCC Ala	GTG Val	GGC Gly	GTG Val	TTC Phe 325	GCA Ala	CCG Pro	CTC Leu	ACT Thr 330	GCG Ala	CAC His	GGG Gly	ACG Thr	CTG Leu 335	CTG Leu	GTC Val	1008
50	AAC Asn	GAC Asp	GTC Val	CTC Leu 340	GCC Ala	TCC Ser	TGC Cys	TAC Tyr	GCG Ala 345	GTT Val	CTA Leu	GAG Glu	AGT Ser 350	CAC His	CAG Gln	TGG Trp	1056
55	GCC Ala	CAC His	CGC Arg 355	GCC Ala	TTC Phe	GCC Ala	CCT Pro	TTG Leu 360	CGG Arg	CTG Leu	CTG Leu	CAC His 365	GCG Ala	CTC Leu	GGG Gly	GCT Ala	1104
60	CTG Leu 370	CTC Leu	CCT Pro	GGG Gly	GGT Gly	GCA Ala	GTC Val 375	CAG Gln	CCG Pro	ACT Thr	GGC Gly	ATG Met 380	CAT His	TGG Trp	TAC Tyr	TCT Ser	1152

CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG 1190
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG 48
 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15

CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG 96
 Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30

GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC 144
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC 192
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG 240
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC 288
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC 336
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG 384
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC TCA GAG GAG TCT TTA 432
 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

CAC TAT GAG GGC CGC GCG GTG GAT ATC ACC ACC TCA GAC CGT GAC CGA 480
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg

[illegible]

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(i) SEQUENCE CHARACTERISTICS:

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(A) NAME/KEY: CDS
(B) LOCATION: 1..1314

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT 432
Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
130 135 140

	CGA Arg 145	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr 150	ACG Thr	TCC Ser	GAC Asp	CGG Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly 160	480
5	ATG Met	CTG Leu	GCT Ala	CGC Arg	CTG Leu 165	GCT Ala	GTG Val	GAA Glu	GCA Ala	GGT Gly 170	TTC Phe	GAC Asp	TGG Trp	GTC Val	TAC Tyr 175	TAT Tyr	528
10	GAA Glu	TCC Ser	AAA Lys	GCT Ala 180	CAC His	ATC Ile	CAC His	TGT Cys	TCT Ser 185	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn 190	TCC Ser	GTG Val	576
15	GCG Ala	GCC Ala	AAA Lys 195	TCC Ser	GGC Gly	GGC Gly	TGT Cys	TTC Phe 200	CCG Pro	GGA Gly	TCC Ser	GCC Ala	ACC Thr 205	GTG Val	CAC His	CTG Leu	624
20	GAG Glu	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu 215	GTG Val	AAG Lys	GAC Asp	TTA Leu 220	CGT Arg	CCC Pro	GGA Gly	GAC Asp	CGC Arg	672
25	GTG Val 225	CTG Leu	GCG Ala	GCT Ala	GAC Asp	GAC Asp 230	CAG Gln	GGC Gly	CGG Arg	CTG Leu 235	CTG Leu 235	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu 240	720
	ACC Thr	TTC Phe	CTG Leu	GAC Asp	CGC Arg 245	GAC Asp	GAA Glu	GGC Gly	GCC Ala	AAG Lys 250	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val 255	ATC Ile	768
30	GAG Glu	ACG Thr	CTG Leu	GAG Glu 260	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu 265	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	816
35	CTC Leu	TTC Phe	GTG Val 275	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp 280	TCG Ser	GGG Gly	CCC Pro	ACG Thr	CCC Pro 285	GGG Gly	CCA Pro	AGC Ser	864
40	GCG Ala 290	CTC Leu	TTT Phe	GCC Ala	AGC Ser	CGC Arg	GTG Val 295	CGC Arg	CCC Pro	GGG Gly	CAG Gln 300	CGC Arg	GTG Val	TAC Tyr	GTG Val	GTG Val	912
45	GCT Ala 305	GAA Glu	CGC Arg	GGC Gly	GGG Gly	GAC Asp 310	CGC Arg	CGG Arg	CTG Leu	CTG Leu	CCC Pro 315	GCC Ala	GCG Ala	GTG Val	CAC His	AGC Ser 320	960
	GTG Val	ACG Thr	CTG Leu	CGA Arg 325	GAG Glu	GAG Glu	GAG Glu	GCG Ala	GGC Gly	GCG Ala 330	TAC Tyr	GCG Ala	CCG Pro	CTC Leu	ACG Thr 335	GCG Ala	1008
50	CAC His	GGC Gly	ACC Thr	ATT Ile 340	CTC Leu	ATC Ile	AAC Asn	CGG Arg	GTG Val 345	CTC Leu	GCC Ala	TCG Ser	TGC Cys	TAC Tyr 350	GCT Ala	GTC Val	1056
55	ATC Ile	GAG Glu	GAG Glu 355	CAC His	AGC Ser	TGG Trp	GCA Ala	CAC His 360	CGG Arg	GCC Ala	TTC Phe	GCG Ala	CCT Pro 365	TTC Phe	CGC Arg	CTG Leu	1104
60	GCG Ala 370	CAC His	GCG Ala	CTG Leu	CTG Leu	GCC Ala	GCG Ala 375	CTG Leu	GCA Ala	CCC Pro	GCC Ala 380	CGC Arg	ACG Thr	GAC Asp	GGC Gly	GGG Gly	1152

	GGC	GGG	GGC	AGC	ATC	CCT	GCA	GCG	CAA	TCT	GCA	ACG	GAA	GCG	AGG	GGC	1200
	Gly	Gly	Gly	Ser	Ile	Pro	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly	
	385					390					395					400	
5	GCG	GAG	CCG	ACT	GCG	GGC	ATC	CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAC	1248
	Ala	Glu	Pro	Thr	Ala	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His	
					405				410						415		
10	ATT	GGC	ACC	TGG	CTG	TTG	GAC	AGC	GAG	ACC	ATG	CAT	CCC	TTG	GGA	ATG	1296
	Ile	Gly	Thr	Trp	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met	
				420					425					430			
	GCG	GTC	AAG	TCC	AGC	TG											1313
15	Ala	Val	Lys	Ser	Ser												
			435														
	(2) INFORMATION FOR SEQ ID NO:5:																
20	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 1256 base pairs																
	(B) TYPE: nucleic acid																
	(C) STRANDEDNESS: both																
	(D) TOPOLOGY: linear																
25	(ii) MOLECULE TYPE: cDNA																
	(ix) FEATURE:																
30	(A) NAME/KEY: CDS																
	(B) LOCATION: 1..1257																
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:																
35	ATG	CGG	CTT	TTG	ACG	AGA	GTG	CTG	CTG	GTG	TCT	CTT	CTC	ACT	CTG	TCC	48
	Met	Arg	Leu	Leu	Thr	Arg	Val	Leu	Leu	Val	Ser	Leu	Leu	Thr	Leu	Ser	
	1				5					10					15		
40	TTG	GTG	GTG	TCC	GGA	CTG	GCC	TGC	GGT	CCT	GGC	AGA	GGC	TAC	GGC	AGA	96
	Leu	Val	Val	Ser	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Tyr	Gly	Arg	
				20					25					30			
45	AGA	AGA	CAT	CCG	AAG	AAG	CTG	ACA	CCT	CTC	GCC	TAC	AAG	CAG	TTC	ATA	144
	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
			35					40					45				
50	CCT	AAT	GTC	GCG	GAG	AAG	ACC	TTA	GGG	GCC	AGC	GGC	AGA	TAC	GAG	GGC	192
	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	
		50					55					60					
55	AAG	ATA	ACG	CGC	AAT	TCG	GAG	AGA	TTT	AAA	GAA	CTT	ACT	CCA	AAT	TAC	240
	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65					70				75						80	
	AAT	CCC	GAC	ATT	ATC	TTT	AAG	GAT	GAG	GAG	AAC	ACG	GGA	GCG	GAC	AGG	288
	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
					85				90						95		
60	CTC	ATG	ACA	CAG	AGA	TGC	AAA	GAC	AAG	CTG	AAC	TCG	CTG	GCC	ATC	TCT	336
	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	

	100										105					110					
5	GTA Val	ATG Met	AAC Asn 115	CAC His	TGG Trp	CCA Pro	GGG Gly	GTT Val 120	AAG Lys	CTG Leu	CGT Arg	GTG Val	ACA Thr 125	GAG Glu	GGC Gly	TGG Trp	384				
10	GAT Asp 130	GAG Glu	GAC Asp	GGT Gly	CAC His	CAT His	TTT Phe 135	GAA Glu	GAA Glu	TCA Ser	CTC Leu	CAC His 140	TAC Tyr	GAG Glu	GGA Gly	AGA Arg	432				
15	GCT Ala 145	GTT Val	GAT Asp	ATT Ile	ACC Thr 150	ACC Thr 150	TCT Ser	GAC Asp	CGA Arg	GAC Asp	AAG Lys 155	AGC Ser	AAA Lys	TAC Tyr	GGG Gly	ACA Thr 160	480				
20	CTG Leu	TCT Ser	CGC Arg	CTA Leu	GCT Ala 165	GTG Val	GAG Glu	GCT Ala	GGA Gly	TTT Phe 170	GAC Asp	TGG Trp	GTC Val	TAT Tyr	TAC Tyr 175	GAG Glu	528				
25	TCC Ser	AAA Lys	GCC Ala 180	CAC His	ATT Ile	CAT His	TGC Cys	TCT Ser	GTC Val 185	AAA Lys	GCA Ala	GAA Glu	AAT Asn	TCG Ser 190	GTT Val	GCT Ala	576				
30	GCG Ala	AAA Lys	TCT Ser 195	GGG Gly	GGC Gly	TGT Cys	TTC Phe	CCA Pro 200	GGT Gly	TCG Ser	GCT Ala	CTG Leu	GTC Val 205	TCG Ser	CTC Leu	CAG Gln	624				
35	GAC Asp 210	GGA Gly	GGA Gly	CAG Gln	AAG Lys	GCC Ala	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AAC Asn	CCC Pro 220	GGA Gly	GAC Asp	AAG Lys	GTG Val	672				
40	CTG Leu 225	GCG Ala	GCA Ala	GAC Asp	AGC Ser	GCG Ala 230	GGA Gly	AAC Asn	CTG Leu	GTG Val	TTC Phe 235	AGC Ser	GAC Asp	TTC Phe	ATC Ile	ATG Met 240	720				
45	TTC Phe	ACA Thr	GAC Asp	CGA Arg	GAC Asp 245	TCC Ser	ACG Thr	ACG Thr	CGA Arg	CGT Arg 250	GTG Val	TTT Phe	TAC Tyr	GTC Val	ATA Ile 255	GAA Glu	768				
50	ACG Thr	CAA Gln	GAA Glu	CCC Pro 260	GTT Val	GAA Glu	AAG Lys	ATC Ile	ACC Thr 265	CTC Leu	ACC Thr	GCC Ala	GCT Ala	CAC His 270	CTC Leu	CTT Leu	816				
55	TTT Phe	GTC Val	CTC Leu 275	GAC Asp	AAC Asn	TCA Ser	ACG Thr	GAA Glu 280	GAT Asp	CTC Leu	CAC His	ACC Thr 285	ATG Met	ACC Thr	GCC Ala	GCG Ala	864				
60	TAT Tyr	GCC Ala 290	AGC Ser	AGT Ser	GTC Val	AGA Arg	GCC Ala 295	GGA Gly	CAA Gln	AAG Lys	GTG Val	ATG Met 300	GTT Val	GTT Val	GAT Asp	GAT Asp	912				
65	AGC Ser 305	GGT Gly	CAG Gln	CTT Leu	AAA Lys	TCT Ser 310	GTC Val	ATC Ile	GTG Val	CAG Gln	CGG Arg 315	ATA Ile	TAC Tyr	ACG Thr	GAG Glu	GAG Glu 320	960				
70	CAG Gln	CGG Arg	GGC Gly	TCG Ser	TTC Phe 325	GCA Ala	CCA Pro	GTG Val	ACT Thr	GCA Ala 330	CAT His	GGG Gly	ACC Thr	ATT Ile	GTG Val 335	GTC Val	1008				
75	GAC Asp	AGA Arg	ATA Ile 340	CTG Leu	GCG Ala	TCC Ser	TGT Cys	TAC Tyr	GCC Ala 345	GTA Val	ATA Ile	GAG Glu	GAC Asp	CAG Gln 350	GGG Gly	CTT Leu	1056				

5 GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA 1104
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
355 360 365

10 TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC 1152
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
370 375 380

15 AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG 1200
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385 390 395 400

20 TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC 1248
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
405 410 415

TCA AGC TG 1256
Ser Ser

(2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1425

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG 48
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
1 5 10 15

45 CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG 96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

50 AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC 144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

55 CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG 192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

60 AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC 240
Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGA GCG GAC AGG 288

	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg	
5	CTG Leu	ATG Met	ACT Thr	CAG Gln 100	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys 105	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala 110	ATC Ile	TCG Ser	336
10	GTG Val	ATG Met	AAC Asn 115	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val 120	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr 125	GAG Glu	GGC Gly	TGG Trp	384
15	GAC Asp	GAA Glu 130	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser 135	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His 140	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432
20	GCA Ala 145	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr 150	TCT Ser	GAC Asp	CGC Arg	GAC Asp 155	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met 160	480
25	CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala 165	GTG Val	GAG Glu	GCC Ala	GGC Gly 170	TTC Phe	GAC Asp	TGG Trp	GTG Val	TAC Tyr	TAC Tyr 175	GAG Glu	528
30	TCC Ser	AAG Lys	GCA Ala	CAT His 180	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val 185	AAA Lys	GCA Ala	GAG Glu	AAC Asn	TCG Ser 190	GTG Val	GCG Ala	576
35	GCC Ala	AAA Lys	TCG Ser 195	GGA Gly	GGC Gly	TGC Cys	TTC Phe 200	CCG Pro	GGC Gly	TCG Ser	GCC Ala	ACG Thr	GTG Val 205	CAC His	CTG Leu	GAG Glu	624
40	CAG Gln 210	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val 215	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro 220	GGG Gly	GAC Asp	CGC Arg	GTG Val	672
45	CTG Leu 225	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln 230	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr 235	AGC Ser	GAC Asp	TTC Phe	CTC Leu	ACT Thr 240	720
50	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp 245	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys 250	GTC Val	TTC Phe	TAC Tyr	GTG Val	ATC Ile 255	GAG Glu	768
55	ACG Thr	CGG Arg	GAG Glu	CCG Pro 260	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu 265	CTC Leu	ACC Thr	GCC Ala	GCG Ala 270	CAC His	CTG Leu	CTC Leu	816
60	TTT Phe	GTG Val	GCG Ala 275	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser 280	GCC Ala	ACC Thr	GGG Gly	GAG Glu	CCC Pro 285	GAG Glu	GCG Ala	TCC Ser	864
65	TCG Ser	GGC Gly 290	TCG Ser	GGG Gly	CCG Pro	CCT Pro	TCC Ser 295	GGG Gly	GGC Gly	GCA Ala	CTG Leu	GGG Gly 300	CCT Pro	CGG Arg	GCG Ala	CTG Leu	912
70	TTC Phe 305	GCC Ala	AGC Ser	CGC Arg	GTG Val	CGC Arg 310	CCG Pro	GGC Gly	CAG Gln	CGC Arg	GTG Val 315	TAC Tyr	GTG Val	GTG Val	GCC Ala	GAG Glu 320	960
75	CGT Arg	GAC Asp	GGG Gly	GAC Asp	CGC Arg	CGG Arg	CTC Leu	CTG Leu	CCC Pro	GCC Ala	GCT Ala	GTG Val	CAC His	AGC Ser	GTG Val	ACC Thr	1008

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATCAGCCCA CCAGGAGACC TCGCCCGCCG CTCCCCGGG CTCCCCGGCC ATG TCT 56
Met Ser
1

	CCC	GCC	CGG	CTC	CGG	CCC	CGA	CTG	CAC	TTC	TGC	CTG	GTC	CTG	TTG	CTG	104
	Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu	Leu	Leu	
5			5					10					15				
	CTG	CTG	GTG	GTG	CCC	GCG	GCA	TGG	GGC	TGC	GGG	CCG	GGT	CGG	GTG	GTG	152
	Leu	Leu	Val	Val	Pro	Ala	Ala	Trp	Gly	Cys	Gly	Pro	Gly	Arg	Val	Val	
		20					25					30					
10	GGC	AGC	CGC	CGG	CGA	CCG	CCA	CGC	AAA	CTC	GTG	CCG	CTC	GCC	TAC	AAG	200
	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	Tyr	Lys	
	35					40					45					50	
15	CAG	TTC	AGC	CCC	AAT	GTG	CCC	GAG	AAG	ACC	CTG	GGC	GCC	AGC	GGA	CGC	248
	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
					55					60					65		
20	TAT	GAA	GGC	AAG	ATC	GCT	CGC	AGC	TCC	GAG	CGC	TTC	AAG	GAG	CTC	ACC	296
	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
				70					75					80			
25	CCC	AAT	TAC	AAT	CCA	GAC	ATC	ATC	TTC	AAG	GAC	GAG	GAG	AAC	ACA	GGC	344
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
			85					90					95				
	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGC	CTG	AAC	TCG	CTG	392
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	Ser	Leu	
		100					105					110					
30	GCT	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGT	GTG	AAG	CTG	CGG	GTG	ACC	440
	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115					120					125					130	
35	GAG	GGC	TGG	GAC	GAG	GAC	GGC	CAC	CAC	TCA	GAG	GAG	TCC	CTG	CAT	TAT	488
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
					135					140					145		
40	GAG	GGC	CGC	GCG	GTG	GAC	ATC	ACC	ACA	TCA	GAC	CGC	GAC	CGC	AAT	AAG	536
	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	
				150					155					160			
45	TAT	GGA	CTG	CTG	GCG	CGC	TTG	GCA	GTG	GAG	GCC	GGC	TTT	GAC	TGG	GTG	584
	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
			165				170						175				
	TAT	TAC	GAG	TCA	AAG	GCC	CAC	GTG	CAT	TGC	TCC	GTC	AAG	TCC	GAG	CAC	632
	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
		180					185					190					
50	TCG	GCC	GCA	GCC	AAG	ACG	GGC	GGC	TGC	TTC	CCT	GCC	GGA	GCC	CAG	GTA	680
	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
	195					200					205				210		
55	CGC	CTG	GAG	AGT	GGG	GCG	CGT	GTG	GCC	TTG	TCA	GCC	GTG	AGG	CCG	GGA	728
	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
					215					220					225		
60	GAC	CGT	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	AGC	CCC	ACC	TTC	AGC	GAT	776
	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
				230					235					240			

10504400723550

	GTG CTC ATT TTC CTG GAC CGC GAG CCC CAC AGG CTG AGA GCC TTC CAG	824
	Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln	
	245 250 255	
5	GTC ATC GAG ACT CAG GAC CCC CCA CGC CGC CTG GCA CTC ACA CCC GCT	872
	Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala	
	260 265 270	
10	CAC CTG CTC TTT ACG GCT GAC AAT CAC ACG GAG CCG GCA GCC CGC TTC	920
	His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe	
	275 280 285 290	
15	CGG GCC ACA TTT GCC AGC CAC GTG CAG CCT GGC CAG TAC GTG CTG GTG	968
	Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val	
	295 300 305	
20	GCT GGG GTG CCA GGC CTG CAG CCT GCC CGC GTG GCA GCT GTC TCT ACA	1016
	Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr	
	310 315 320	
25	CAC GTG GCC CTC GGG GCC TAC GCC CCG CTC ACA AAG CAT GGG ACA CTG	1064
	His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu	
	325 330 335	
30	GTG GTG GAG GAT GTG GTG GCA TCC TGC TTC GCG GCC GTG GCT GAC CAC	1112
	Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His	
	340 345 350	
35	CAC CTG GCT CAG TTG GCC TTC TGG CCC CTG AGA CTC TTT CAC AGC TTG	1160
	His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu	
	355 360 365 370	
40	GCA TGG GGC AGC TGG ACC CCG GGG GAG GGT GTG CAT TGG TAC CCC CAG	1208
	Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln	
	375 380 385	
45	CTG CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC	1256
	Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His	
	390 395 400	
50	CCA CTG GGC ATG TCC GGG GCA GGG AGC TGAAAGGACT CCACCGCTGC	1303
	Pro Leu Gly Met Ser Gly Ala Gly Ser	
	405 410	
55	CCTCCTGGAA CTGCTGTACT GGGTCCAGAA GCCTCTCAGC CAGGAGGGAG CTGGCCCTGG	1363
	AAGGGACCTG AGCTGGGGGA CACTGGCTCC TGCCATCTCC TCTGCCATGA AGATACACCA	1423
	TTGAGACTTG ACTGGGCAAC ACCAGCGTCC CCCACCCGCG TCGTGGTGTA GTCATAGAGC	1483
	TGCAAGCTGA GCTGGCGAGG GGATGGTTGT TGACCCCTCT CTCCTAGAGA CCTTGAGGCT	1543
	GGCAGGCGCA CTCCCAACTC AGCCTGCTCT CACTACGAGT TTTCATACTC TGCCTCCCCC	1603
	ATTGGGAGGG CCCATTCCC	1622

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid

60

(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15	ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG	48
	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
20	GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG	96
	Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
	20 25 30	
25	CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT	144
	Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
	35 40 45	
30	GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG	192
	Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
	50 55 60	
35	GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC	240
	Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
	65 70 75 80	
40	TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC	288
	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
	85 90 95	
45	CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT	336
	Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	
	100 105 110	
50	GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC	384
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
55	TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC	432
	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
	130 135 140	
60	CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG	480
	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
	145 150 155 160	
65	TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC	528
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
	165 170 175	
70	GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG	576
	Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
	180 185 190	

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1248

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC	48
	Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	
	1 5 10 15	
15	AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT	96
	Ser Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
	20 25 30	
20	TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG	144
	Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
25	CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	
	50 55 60	
30	TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	
	65 70 75 80	
35	CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	
	85 90 95	
40	GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG	336
	Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	
	100 105 110	
45	GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT	384
	Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	
50	GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT	432
	Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	
	130 135 140	
55	GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
	145 150 155 160	
60	TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC	528
	Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
	165 170 175	
65	TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT	576
	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
	180 185 190	
70	TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG	624
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	

	195	200	205	
5	ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220			672
10	GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235			720
15	TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255			768
20	GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270			816
25	CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275 280 285			864
30	ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290 295 300			912
35	GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305 310 315 320			960
40	GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325 330 335			1008
45	ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340 345 350			1056
50	AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355 360 365			1104
55	ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu 370 375 380			1152
60	GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp 385 390 395 400			1200
65	CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser 405 410 415			1248
70	TGA			1251

(2) INFORMATION FOR SEQ ID NO:10:

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10 Met Val Glu Met Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
1 5 10 15
Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
20 25 30
15 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
50 55 60
20 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
65 70 75 80
25 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85 90 95
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
100 105 110
30 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
130 135 140
35 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
145 150 155 160
40 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
180 185 190
45 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
195 200 205
His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
210 215 220
50 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
225 230 235 240
Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
245 250 255
Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
260 265 270
60 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
275 280 285

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	Ser	Thr	Ser	Gly	Gln	Ala	Leu	Phe	Ala	Ser	Asn	Val	Lys	Pro	Gly	Gln
	290						295					300				
5	Arg	Val	Tyr	Val	Leu	Gly	Glu	Gly	Gly	Gln	Gln	Leu	Leu	Pro	Ala	Ser
	305					310					315					320
	Val	His	Ser	Val	Ser	Leu	Arg	Glu	Glu	Ala	Ser	Gly	Ala	Tyr	Ala	Pro
					325					330					335	
10	Leu	Thr	Ala	Gln	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys
				340					345					350		
15	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	Trp	Ala	Phe	Ala	Pro
			355					360					365			
	Phe	Arg	Leu	Ala	Gln	Gly	Leu	Leu	Ala	Ala	Leu	Cys	Pro	Asp	Gly	Ala
	370						375					380				
20	Ile	Pro	Thr	Ala	Ala	Thr	Thr	Thr	Thr	Gly	Ile	His	Trp	Tyr	Ser	Arg
	385					390					395					400
	Leu	Leu	Tyr	Arg	Ile	Gly	Ser	Trp	Val	Leu	Asp	Gly	Asp	Ala	Leu	His
					405					410					415	
25	Pro	Leu	Gly	Met	Val	Ala	Pro	Ala	Ser							
				420					425							
30	(2) INFORMATION FOR SEQ ID NO:11:															
	(i) SEQUENCE CHARACTERISTICS:															
	(A) LENGTH: 396 amino acids															
	(B) TYPE: amino acid															
35	(D) TOPOLOGY: linear															
	(ii) MOLECULE TYPE: protein															
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:															
	Met	Ala	Leu	Pro	Ala	Ser	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
	1				5					10					15	
45	Ala	Leu	Ser	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
50	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
	50						55					60				
55	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70					75					80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
60	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile

	100	105	110
	Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly		
	115	120	125
5	Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly		
	130	135	140
10	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly		
	145	150	155
	Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr		
		165	170
15	Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu		
		180	185
	Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu		
		195	200
20	Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp		
		210	215
25	Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu		
		225	230
	Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val		
		245	250
30	Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu		
		260	265
	Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro		
		275	280
35	Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly		
		290	295
40	Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu		
		305	310
	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val		
		325	330
45	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp		
		340	345
	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala		
		355	360
50	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser		
		370	375
55	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly		
		385	390

(2) INFORMATION FOR SEQ ID NO:12:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30
15 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45
20 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80
25 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110
30 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125
35 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160
40 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
165 170 175
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190
45 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195 200 205
50 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
210 215 220
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225 230 235 240
55 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245 250 255
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260 265 270
60 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala

2

[REDACTED]

Ala Val Lys Ser Ser
435

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15
Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
25 35 40 45
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60
Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
30 65 70 75 80
Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95
Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
35 100 105 110
Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
40 115 120 125
Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140
Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
45 145 150 155 160
Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
50 180 185 190
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
55 195 200 205
Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
210 215 220
Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
60 225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
245 250 255

5 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
275 280 285

10 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
290 295 300

15 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
325 330 335

20 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
355 360 365

25 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
370 375 380

30 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
405 410 415

35 Ser Ser

40 (2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
1 5 10 15

55 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

60 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly

	50					55					60					
	Lys 65	Ile	Ser	Arg	Asn	Ser 70	Glu	Arg	Phe	Lys	Glu 75	Leu	Thr	Pro	Asn	Tyr 80
5	Asn	Pro	Asp	Ile	Ile 85	Phe	Lys	Asp	Glu	Glu 90	Asn	Thr	Gly	Ala	Asp 95	Arg
10	Leu	Met	Thr	Gln 100	Arg	Cys	Lys	Asp	Lys 105	Leu	Asn	Ala	Leu	Ala 110	Ile	Ser
	Val	Met	Asn 115	Gln	Trp	Pro	Gly	Val 120	Lys	Leu	Arg	Val	Thr 125	Glu	Gly	Trp
15	Asp	Glu 130	Asp	Gly	His	His	Ser 135	Glu	Glu	Ser	Leu	His 140	Tyr	Glu	Gly	Arg
20	Ala 145	Val	Asp	Ile	Thr	Thr 150	Ser	Asp	Arg	Asp	Arg 155	Ser	Lys	Tyr	Gly	Met 160
	Leu	Ala	Arg	Leu	Ala 165	Val	Glu	Ala	Gly	Phe 170	Asp	Trp	Val	Tyr	Tyr 175	Glu
25	Ser	Lys	Ala	His 180	Ile	His	Cys	Ser	Val 185	Lys	Ala	Glu	Asn	Ser 190	Val	Ala
	Ala	Lys	Ser 195	Gly	Gly	Cys	Phe	Pro 200	Gly	Ser	Ala	Thr	Val 205	His	Leu	Glu
30	Gln	Gly 210	Gly	Thr	Lys	Leu	Val 215	Lys	Asp	Leu	Ser	Pro 220	Gly	Asp	Arg	Val
35	Leu 225	Ala	Ala	Asp	Asp	Gln 230	Gly	Arg	Leu	Leu	Tyr 235	Ser	Asp	Phe	Leu	Thr 240
	Phe	Leu	Asp	Arg	Asp 245	Asp	Gly	Ala	Lys	Lys 250	Val	Phe	Tyr	Val	Ile 255	Glu
40	Thr	Arg	Glu	Pro 260	Arg	Glu	Arg	Leu	Leu 265	Leu	Thr	Ala	Ala 270	His	Leu	Leu
	Phe	Val	Ala 275	Pro	His	Asn	Asp	Ser 280	Ala	Thr	Gly	Glu	Pro 285	Glu	Ala	Ser
45	Ser	Gly 290	Ser	Gly	Pro	Pro	Ser 295	Gly	Gly	Ala	Leu	Gly 300	Pro	Arg	Ala	Leu
50	Phe 305	Ala	Ser	Arg	Val	Arg 310	Pro	Gly	Gln	Arg	Val 315	Tyr	Val	Val	Ala	Glu 320
	Arg	Asp	Gly	Asp	Arg 325	Arg	Leu	Leu	Pro	Ala 330	Ala	Val	His	Ser	Val 335	Thr
55	Leu	Ser	Glu	Glu 340	Ala	Ala	Gly	Ala	Tyr 345	Ala	Pro	Leu	Thr	Ala 350	Gln	Gly
	Thr	Ile	Leu 355	Ile	Asn	Arg	Val	Leu 360	Ala	Ser	Cys	Tyr	Ala 365	Val	Ile	Glu
60	Glu	His 370	Ser	Trp	Ala	His	Arg 375	Ala	Phe	Ala	Pro	Phe 380	Arg	Leu	Ala	His

60

	165	170	175
	Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser		
	180	185	190
5	Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala		
	195	200	205
10	Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg		
	210	215	220
	Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe		
	225	230	235
15	Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala		
	245	250	255
	Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr		
	260	265	270
20	Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala		
	275	280	285
	Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val		
	290	295	300
25	Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val		
	305	310	315
30	Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly		
	325	330	335
	Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala		
	340	345	350
35	Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His		
	355	360	365
	Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr		
	370	375	380
40	Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser		
	385	390	395
45	Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser		
	405	410	

(2) INFORMATION FOR SEQ ID NO:17:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

60	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
	1 5 10 15

	Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
				20					25					30		
5	Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
			35					40					45			
	Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
		50					55					60				
10	Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
	65					70					75					80
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
15	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
				100					105					110		
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
20			115					120					125			
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130						135					140				
25	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145					150					155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
					165					170					175	
30	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
35			195					200					205			
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210						215					220				
40	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
	225					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
					245					250					255	
45	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
50			275					280					285			
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
		290					295					300				
55	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
	305					310					315					320
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
					325					330					335	
60	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

25	Met 1	Asp	Val	Arg	Leu 5	His	Leu	Lys	Gln	Phe 10	Ala	Leu	Leu	Cys	Phe 15	Ile
	Ser	Leu	Leu	Leu 20	Thr	Pro	Cys	Gly	Leu 25	Ala	Cys	Gly	Pro	Gly 30	Arg	Gly
30	Tyr	Gly	Lys 35	Arg	Arg	His	Pro	Lys 40	Lys	Leu	Thr	Pro	Leu 45	Ala	Tyr	Lys
	Gln	Phe 50	Ile	Pro	Asn	Val	Ala 55	Glu	Lys	Thr	Leu	Gly 60	Ala	Ser	Gly	Lys
	Tyr 65	Glu	Gly	Lys	Ile	Thr 70	Arg	Asn	Ser	Glu	Arg 75	Phe	Lys	Glu	Leu	Ile 80
40	Pro	Asn	Tyr	Asn 85	Pro	Asp	Ile	Ile	Phe	Lys 90	Asp	Glu	Glu	Asn	Thr 95	Asn
	Ala	Asp	Arg	Leu 100	Met	Thr	Lys	Arg	Cys 105	Lys	Asp	Lys	Leu	Asn 110	Ser	Leu
45	Ala	Ile	Ser 115	Val	Met	Asn	His	Trp 120	Pro	Gly	Val	Lys	Leu 125	Arg	Val	Thr
	Glu	Gly 130	Trp	Asp	Glu	Asp	Gly 135	His	His	Leu	Glu	Glu 140	Ser	Leu	His	Tyr
50	Glu 145	Gly	Arg	Ala	Val	Asp 150	Ile	Thr	Thr	Ser	Asp 155	Arg	Asp	Lys	Ser	Lys 160
	Tyr	Gly	Met	Leu 165	Ser	Arg	Leu	Ala	Val	Glu 170	Ala	Gly	Phe	Asp	Trp 175	Val
55	Tyr	Tyr	Glu 180	Ser	Lys	Ala	His	Ile	His 185	Cys	Ser	Val	Lys	Ala 190	Glu	Asn
60	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Gly	Thr	Val

	195	200	205
5	Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220		
	Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235 240		
10	Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255		
	Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270		
15	His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275 280 285		
	Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290 295 300		
20	Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305 310 315 320		
	Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325 330 335		
25	Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340 345 350		
30	Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355 360 365		
	Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu 370 375 380		
35	Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp 385 390 395 400		
40	Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser 405 410 415		

(2) INFORMATION FOR SEQ ID NO:19:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1413

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT AAC CAC AGC TCA GTG CCT TGG GCC AGT GCC GCC AGT GTC ACC

	Met 1	Asp	Asn	His	Ser 5	Ser	Val	Pro	Trp	Ala 10	Ser	Ala	Ala	Ser	Val 15	Thr	
5	TGT Cys	CTC Leu	TCC Ser	CTG Leu 20	GGA Gly	TGC Cys	CAA Gln	ATG Met	CCA Pro 25	CAG Gln	TTC Phe	CAG Gln	TTC Phe	CAG Gln 30	TTC Phe	CAG Gln	96
10	CTC Leu	CAA Gln	ATC Ile 35	CGC Arg	AGC Ser	GAG Glu	CTC Leu	CAT His 40	CTC Leu	CGC Arg	AAG Lys	CCC Pro	GCA Ala 45	AGA Arg	AGA Arg	ACG Thr	144
15	CAA Gln	ACG Thr 50	ATG Met	CGC Arg	CAC His	ATT Ile	GCG Ala 55	CAT His	ACG Thr	CAG Gln	CGT Arg	TGC Cys 60	CTC Leu	AGC Ser	AGG Arg	CTG Leu	192
20	ACC Thr 65	TCT Ser	CTG Leu	GTG Val	GCC Ala	CTG Leu 70	CTG Leu	CTG Leu	ATC Ile	GTC Val	TTG Leu 75	CCG Pro	ATG Met	GTC Val	TTT Phe	AGC Ser 80	240
25	CCG Pro	GCT Ala	CAC His	AGC Ser	TGC Cys 85	GGT Gly	CCT Pro	GGC Gly	CGA Arg	GGA Gly 90	TTG Leu	GGT Gly	CGT Arg	CAT His	AGG Arg 95	GCG Ala	288
30	CGC Arg	AAC Asn	CTG Leu 100	TAT Tyr	CCG Pro	CTG Leu	GTC Val	CTC Leu	AAG Lys 105	CAG Gln	ACA Thr	ATT Ile	CCC Pro	AAT Asn 110	CTA Leu	TCC Ser	336
35	GAG Glu	TAC Tyr	ACG Thr 115	AAC Asn	AGC Ser	GCC Ala	TCC Ser	GGA Gly 120	CCT Pro	CTG Leu	GAG Glu	CGT Gly	GTG Val 125	ATC Ile	CGT Arg	CGG Arg	384
40	GAT Asp	TCG Ser 130	CCC Pro	AAA Lys	TTC Phe	AAG Lys	GAC Asp 135	CTC Leu	GTG Val	CCC Pro	AAC Asn	TAC Tyr 140	AAC Asn	AGG Arg	GAC Asp	ATC Ile	432
45	CTT Leu 145	TTC Phe	CGT Arg	GAC Asp	GAG Glu	GAA Glu 150	GGC Gly	ACC Thr	GGA Gly	GCG Ala	GAT Asp 155	GGC Gly	TTG Leu	ATG Met	AGC Ser	AAG Lys 160	480
50	CGC Arg	TGC Cys	AAG Lys	GAG Glu	AAG Lys 165	CTA Leu	AAC Asn	GTG Val	CTG Leu 170	GCC Ala	TAC Tyr	TCG Ser	GTG Val	ATG Met	AAC Asn 175	GAA Glu	528
55	TGG Trp	CCC Pro	GGC Gly 180	ATC Ile	CGG Arg	CTG Leu	CTG Leu	GTC Val	ACC Thr 185	GAG Glu	AGC Ser	TGG Trp	GAC Asp 190	GAG Glu	GAC Asp	TAC Tyr	576
60	CAT His	CAC His	GGC Gly 195	CAG Gln	GAG Glu	TCG Ser	CTC Leu	CAC His 200	TAC Tyr	GAG Glu	GGC Gly	CGA Arg	GCG Ala 205	GTG Val	ACC Thr	ATT Ile	624
65	GCC Ala 210	ACC Thr	TCC Ser	GAT Asp	CGC Arg	GAC Asp	CAG Gln 215	TCC Ser	AAA Lys	TAC Tyr	GGC Gly	ATG Met 220	CTC Leu	GCT Ala	CGC Arg	CTG Leu	672
70	GCC Ala 225	GTC Val	GAG Glu	GCT Ala	GGA Gly	TTC Phe 230	GAT Asp	TGG Trp	GTC Val	TCC Ser	TAC Tyr 235	GTC Val	AGC Ser	AGG Arg	CGC Arg	CAC His 240	720
75	ATC Ile	TAC Tyr	TGC Cys	TCC Ser	GTC Val	AAG Lys	TCA Ser	GAT Asp	TCG Ser	TCG Ser	ATC Ile	AGT Ser	TCC Ser	CAC His	GTG Val	CAC His	768

[illegible]

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

10	Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr
	1				5					10					15	
	Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln
				20					25					30		
15	Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr
			35					40					45			
	Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu
		50					55					60				
20	Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser
	65					70				75						80
25	Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala
					85					90					95	
	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser
				100					105					110		
30	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg
			115					120					125			
	Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile
		130					135					140				
35	Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys
	145					150					155					160
40	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu
					165					170					175	
	Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr
				180					185					190		
45	His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile
			195					200					205			
	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu
		210					215					220				
50	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His
	225					230					235					240
55	Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His
					245					250					255	
	Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg
				260					265					270		
60	Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr

275 280 285

Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
290 295 300

5 Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
305 310 315 320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
10 325 330 335

Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
340 345 350

15 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
355 360 365

Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
370 375 380

20 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385 390 395 400

Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
25 405 410 415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
420 425 430

30 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
35 450 455 460

Pro Gln Ser Trp Arg His Asp
465 470

40 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

55 Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
1 5 10 15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

60 Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
50 55 60

5 Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

10 Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
115 120 125

15 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
130 135 140

20 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
165 170 175

25 Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
195 200 205

30 Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

35 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

50 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
1 5 10 15

55 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
35 40 45

60 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
50 55 60

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	Phe	Lys	Asp	Glu	Glu	Asn	Xaa	Gly	Ala	Asp	Arg	Leu	Met	Thr	Xaa	Arg	
	65					70					75					80	
5	Cys	Lys	Xaa	Xaa	Xaa	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	
					85					90					95		
	Pro	Gly	Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Xaa	Asp	Glu	Asp	Gly	His	
				100					105					110			
10	His	Xaa	Xaa	Xaa	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Xaa	Asp	Ile	Thr	
			115					120						125			
	Thr	Ser	Asp	Arg	Asp	Xaa	Xaa	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	
15			130				135						140				
	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Xaa	Xaa	His	Xaa	
	145					150					155					160	
20	His	Xaa	Ser	Val	Lys	Xaa	Xaa										
					165												

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